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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/988,982

DATE: 01/26/2002

TIME: 13:58:47

Input Set : N:\Crf3\RULE60\09988982.raw

Output Set: N:\CRF3\01252002\I988982.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Hillman, Jennifer L.

6 Shah, Purvi

7 Murry, Lynn E.

9 (ii) TITLE OF INVENTION: NOVEL HUMAN LYSOPHOSPHOLIPASE

11 (iii) NUMBER OF SEQUENCES: 3

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.

15 (B) STREET: 3174 Porter Drive

16 (C) CITY: Palo Alto

17 (D) STATE: CA

18 (E) COUNTRY: USA

19 (F) ZIP: 94304

ENTERED

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette

23 (B) COMPUTER: IBM Compatible

24 (C) OPERATING SYSTEM: DOS

25 (D) SOFTWARE: FastSEQ for Windows Version 2.0

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/988,982

C--> 29 (B) FILING DATE: 19-Nov-2001

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: 09/213,394

33 (B) FILING DATE:

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Billings, Lucy J.

37 (B) REGISTRATION NUMBER: 36,749

38 (C) REFERENCE/DOCKET NUMBER: PF-0269 US

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 415-855-0555

42 (B) TELEFAX: 415-845-4166

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 208 amino acids

49 (B) TYPE: amino acid

50 (C) STRANDEDNESS: single

51 (D) TOPOLOGY: linear

53 (vii) IMMEDIATE SOURCE:

54 (A) LIBRARY: KIDNNOT19

55 (B) CLONE: 2676650

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

59 Met Cys Gly Asn Asn Met Ser Thr Pro Leu Pro Ala Ile Val Pro Ala

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60      1          5          10          15
61 Ala Arg Lys Ala Thr Ala Ala Val Ile Phe Leu His Gly Leu Gly Asp
62                20                25                30
63 Thr Gly Pro Val Arg Pro Val Thr Leu Asn Met Asn Val Ala Met Pro
64                35                40                45
65 Ser Trp Phe Asp Ile Ile Gly Leu Ser Pro Asp Ser Gln Glu Asp Glu
66                50                55                60
67 Ser Gly Ile Lys Gln Ala Ala Glu Asn Ile Lys Ala Leu Ile Asp Gln
68 65                70                75                80
69 Glu Val Lys Asn Gly Ile Pro Ser Asn Arg Ile Ile Leu Gly Gly Phe
70                85                90                95
71 Ser Gln Gly Gly Ala Leu Ser Leu Tyr Thr Ala Leu Thr Thr Gln Gln
72                100                105                110
W--> 73 Lys Leu Ala Gly Val Thr Ala Leu Ser Phe Leu Leu Pro Leu Arg Xaa
74                115                120                125
75 Ser Phe Pro Gln Gly Pro Ile Gly Gly Ala Asn Arg Asp Ile Ser Ile
76                130                135                140
77 Leu Gln Cys His Gly Asp Cys Asp Pro Leu Val Pro Leu Met Phe Gly
78 145                150                155                160
79 Ser Leu Thr Val Glu Lys Leu Lys Thr Leu Val Asn Pro Ala Asn Val
80                165                170                175
81 Thr Phe Lys Thr Tyr Glu Gly Met Met His Ser Ser Cys Gln Gln Glu
82                180                185                190
83 Met Met Asp Val Lys Gln Phe Ile Asp Lys Leu Leu Pro Pro Ile Asp
84                195                200                205
86 (2) INFORMATION FOR SEQ ID NO: 2:
88     (i) SEQUENCE CHARACTERISTICS:
89         (A) LENGTH: 709 base pairs
90         (B) TYPE: nucleic acid
91         (C) STRANDEDNESS: single
92         (D) TOPOLOGY: linear
94     (vii) IMMEDIATE SOURCE:
95         (A) LIBRARY: KIDNNOT19
96         (B) CLONE: 2676650
98     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
100 GCCGCTCGCA CGCCCTTGGG CCGCGGCCGG GCGCCCGCTC TTCCTTCCGC TTGCGCTGTG      60
101 AGCTGAGGCG GTGTATGTGC GGCAATAACA TGTCAACCCC GCTGCCCCGCC ATCGTGCCCCG      120
102 CCGCCCGGAA GGCCACCGCT GCGGTGATTT TCCTGCATGG ATTGGGAGAT ACTGGGCCTG      180
103 TTAGGCCTGT TACATTAAAT ATGAACGTGG CTATGCCTTC ATGGTTTGAT ATTATTGGGC      240
104 TTTCAACCAGA TTCACAGGAG GATGAATCTG GGATTAAACA GGCAGCAGAA AATATAAAAAG      300
105 CTTTGATTGA TCAAGAAGTG AAGAATGGCA TTCCTTCTAA CAGAATTATT TTGGGAGGGT      360
106 TTTCTCAGGG AGGAGCTTTA TCTTTATATA CTGCCCTTAC CACACAGCAG AAACCTGGCAG      420
107 GTGTCACTGC ACTCAGTTTC TTGCTTCCAC TTCGGGNTTC CTTTCCACAG GKCCTATCG      480
108 GTGGTGCTAA TAGAGATATT TCTATTCTCC AGTGCCACGG GGATTGTGAC CCTTTGGTTC      540
109 CCCTGATGTT TGGTTCTCTT ACGGTGAAA AACTAAAAAC ATTGGTGAAT CCAGCCAATG      600
110 TGACCTTTAA AACCTATGAA GGTATGATGC ACAGTTCGTG TCAACAGGAA ATGATGGATG      660
111 TCAAGCAATT CATTGATAAA CTCCTACCTC CAATTGATTG ACGTCACTA      709
113 (2) INFORMATION FOR SEQ ID NO: 3:
115     (i) SEQUENCE CHARACTERISTICS:

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116      (A) LENGTH: 230 amino acids
117      (B) TYPE: amino acid
118      (C) STRANDEDNESS: single
119      (D) TOPOLOGY: linear
121      (vii) IMMEDIATE SOURCE:
122          (A) LIBRARY: GenBank
123          (B) CLONE: 552244
125      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
127 Met Cys Gly Asn Asn Met Ser Ala Pro Met Pro Ala Val Val Pro Ala
128   1          5          10          15
129 Ala Arg Lys Ala Thr Ala Ala Val Ile Phe Leu His Gly Leu Gly Asp
130          20          25          30
131 Thr Gly His Gly Trp Ala Glu Ala Phe Ala Gly Ile Lys Ser Ser His
132          35          40          45
133 Ile Lys Tyr Ile Cys Pro His Ala Pro Val Met Pro Val Thr Leu Asn
134          50          55          60
135 Met Ser Met Met Met Pro Ser Trp Phe Asp Ile Ile Gly Leu Ser Pro
136          65          70          75          80
137 Asp Ser Gln Glu Asp Glu Ser Gly Ile Lys Gln Ala Ala Glu Thr Val
138          85          90          95
139 Lys Ala Leu Ile Asp Gln Glu Val Lys Asn Gly Ile Pro Ser Asn Arg
140          100         105         110
141 Ile Ile Leu Gly Gly Phe Ser Gln Gly Gly Ala Leu Ser Leu Tyr Thr
142          115         120         125
143 Ala Leu Thr Thr Gln Gln Lys Leu Ala Gly Val Thr Ala Leu Ser Cys
144          130         135         140
145 Trp Leu Pro Leu Arg Ala Ser Phe Ser Gln Gly Pro Ile Asn Ser Ala
146          145         150         155         160
147 Asn Arg Asp Ile Ser Val Leu Gln Cys His Gly Asp Cys Asp Pro Leu
148          165         170         175
149 Val Pro Leu Met Phe Gly Ser Leu Thr Val Glu Arg Leu Lys Gly Leu
150          180         185         190
151 Val Asn Pro Ala Asn Val Thr Phe Lys Val Tyr Glu Gly Met Met His
152          195         200         205
153 Ser Ser Cys Gln Gln Glu Met Met Asp Val Lys Tyr Phe Ile Asp Lys
154          210         215         220
155 Leu Leu Pro Pro Ile Asp
156          225         230

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1